

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/147,346

DATE: 03/22/2000
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Input Set: I147346.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: YISSUM Research Development Company of the Hebrew
2 YARKONI, Shai
3 NECHUSHTAN, Amotz
4 LORBERBOUM-GALSKI, Haya
5 MARIANOVSKI, Irina
6 <120> TITLE OF INVENTION: CHIMERIC TOXINS FOR TARGETED THERAPY
7 <130> FILE REFERENCE: 1268-073
8 <140> CURRENT APPLICATION NUMBER: US/09/147,346
9 <141> CURRENT FILING DATE: 1999-03-01
10 <150> EARLIER APPLICATION NUMBER: PCT\IL97\00180
11 <151> EARLIER FILING DATE: 1996-06-04
12 <160> NUMBER OF SEQ ID NOS: 4
13 <170> SOFTWARE: PatentIn Ver. 2.1
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15 <211> LENGTH: 1152
16 <212> TYPE: DNA
17 <213> ORGANISM: Escherichia coli
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21 actttcaccg gtcacgcgca gccgcgcggc tgggaacaac tggagcagtg cggctatccg 180
22 gtgcagcggc tggtcgcctt ctacctggcg gcgcggtgt cgtggaacca ggtcgaccag 240
23 gtgatccgca acgccctggc cagccccggc agcggcggcg acctgggaga agcgatccgc 300
24 gagcagcggc agcaggcccg tctggccctg acctggccg cgcgcgagag cgagcgcttc 360
25 gtccggcagg gcaccggcaa cgacgaggcc ggcgcgcca acgccgacgt ggtgagcctg 420
26 acctgcccgg tcgcccggcg tgaatgcgcg ggcccggcg acagcggcga cgccctgctg 480
27 gagcgcaact atcccactgg cgcggagtgc ctcggcgacg gcggcgacgt cagcttcagc 540
28 acccgcggca cgcagaactg gacggtggag cggctgctcc aggcgcaccg ccaactggag 600
29 gagcgcggtc atgtgttcgt cggctaccac ggacacctcc tcgaagcggc gcaaagcatc 660
30 gtcttcggcg gggtgcgcg gcgcagccag gacctcgac cgatctggcg cggtttctat 720
31 atcgccggcg atccggcgct ggcctacggc tacgccagg accaggaacc cgacgcacgc 780
32 ggccggatcc gcaacgggtg cctgctgcgg gtctatgtgc cgcgctcgag cctgccgggc 840
33 ttctaccgca ccagcctgac cctggccggc ccggaggcgg cgggcgaggt cgaacggctg 900
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35 cgctgggaga ccattctcgg ctggccgctg gccgagcgca ccgtggtgat tccctcggcg 1020
36 atccccaccg acccgcgcaa cgtcggcggc gacctcgacc cgtccagcat ccccgacaag 1080
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40 <211> LENGTH: 383
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42 <213> ORGANISM: Escherichia coli
43 <400> SEQUENCE: 2
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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/147,346

DATE: 03/22/2000
TIME: 10:17:37

Input Set: I147346.RAW

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45      1      5      10      15
46    Ala His Met Ala Glu Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His
47              20              25              30
48    Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro
49              35              40              45
50    Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu
51              50              55              60
52    Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln
53              65              70              75              80
54    Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly
55              85              90              95
56    Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu
57              100              105              110
58    Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp
59              115              120              125
60    Glu Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val
61              130              135              140
62    Ala Ala Gly Ala Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu
63    145              150              155              160
64    Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp
65              165              170              175
66    Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu
67              180              185              190
68    Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly
69              195              200              205
70    Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly
71              210              215              220
72    Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr
73    225              230              235              240
74    Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu
75              245              250              255
76    Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr
77              260              265              270
78    Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu
79              275              280              285
80    Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
81              290              295              300
82    Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly
83    305              310              315              320
84    Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val
85              325              330              335
86    Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu
87              340              345              350
88    Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro
89              355              360              365
90    Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys
91              370              375              380

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92 <210> SEQ ID NO 3
93 <211> LENGTH: 1869
94 <212> TYPE: DNA

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PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/147,346

DATE: 03/22/2000
TIME: 10:17:37

Input Set: I147346.RAW

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99   ccggccatcg ccgacaccaa cggccagggc gtgctgcact actccatggt cctggagggc 180
100  ggcaacgacg cgctcgagct ggccatcgac aacgccctca gcatcaccag cgacggcctg 240
101  accatccgcc tcgaaggcgg cgctgagccg aacaagccgc tgcgctacag ctacacgcgc 300
102  caggcgcgcg gcaggtggtc gctgaactgg ctggtaccga tcggccacga gaagccctcg 360
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120  ttcggcgggg tgcgcgcgcg cagccaggac ctgcagcgca tctggcgcgg tttctatatc 1440
121  gccggcgatc cggcgctggc ctacggctac gccaggacc aggaaccgca cgcacgcggc 1500
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125  ctggagacca ttctcggtg gccgctggcc gagcgaccg tggtgattcc ctcggcgatc 1740
126  cccaccgacc cgcgcaacgt cggcgcgac ctcgaccgt ccagcatccc cgacaaggaa 1800
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128  ctgaagtaa                                     1869
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130 <211> LENGTH: 622
131 <212> TYPE: PRT
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133 <400> SEQUENCE: 4
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137             20             25             30
138   Arg Ser Ser Arg Met Ser Val Asp Pro Ala Ile Ala Asp Thr Asn Gly
139             35             40             45
140   Gln Gly Val Leu His Tyr Ser Met Val Leu Glu Gly Gly Asn Asp Ala
141             50             55             60
142   Leu Glu Leu Ala Ile Asp Asn Ala Leu Ser Ile Thr Ser Asp Gly Leu
143             65             70             75             80
144   Thr Ile Arg Leu Glu Gly Gly Val Glu Pro Asn Lys Pro Leu Arg Tyr

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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/147,346

DATE: 03/22/2000
TIME: 10:17:37

Input Set: I147346.RAW

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146	Ser Tyr Thr Arg Gln Ala Arg Gly Arg Trp Ser Leu Asn Trp Leu Val						
147		100		105		110	
148	Pro Ile Gly His Glu Lys Pro Ser Asn Ile Lys Val Phe Ile His Glu						
149		115		120		125	
150	Leu Asn Ala Gly Asn Gln Leu Ser His Met Ser Pro Ile Tyr Thr Ile						
151		130		135		140	
152	Glu Met Gly Asp Glu Leu Leu Ala Lys Leu Ala Arg Asp Ala Thr Phe						
153		145		150		155	
154	Phe Val Arg Ala His Glu Ser Asn Glu Met Gln Pro Thr Leu Ala Ile						
155		165		170		175	
156	Ser His Ala Gly Val Ser Val Val Met Ala Gln Thr Gln Pro Arg Arg						
157		180		185		190	
158	Glu Lys Arg Trp Ser Glu Trp Ala Ser Gly Lys Val Leu Cys Leu Leu						
159		195		200		205	
160	Asp Pro Leu Asp Gly Val Tyr Asn Tyr Leu Ala Gln Gln Arg Cys Asn						
161		210		215		220	
162	Leu Asp Asp Thr Trp Glu Gly Lys Ile Tyr Arg Val Leu Ala Gly Asn						
163		225		230		235	
164	Pro Ala Lys His Asp Leu Asp Ile Lys Pro Thr Val Ile Ser Glu Glu						
165		245		250		255	
166	Leu Glu Phe Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln						
167		260		265		270	
168	Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg						
169		275		280		285	
170	Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val						
171		290		295		300	
172	Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val						
173		305		310		315	
174	Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu						
175		325		330		335	
176	Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala						
177		340		345		350	
178	Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu						
179		355		360		365	
180	Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala						
181		370		375		380	
182	Ala Gly Glu Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu						
183		385		390		395	
184	Ala Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val						
185		405		410		415	
186	Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu						
187		420		425		430	
188	Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr						
189		435		440		445	
190	His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val						
191		450		455		460	
192	Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile						
193		465		470		475	
194	Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro						

PAGE: 5

RAW SEQUENCE LISTING
 PATENT APPLICATION US/09/147,346

DATE: 03/22/2000
 TIME: 10:17:37

Input Set: I147346.RAW

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198	Pro	Arg	Ser	Ser	Leu	Pro
199				515		520
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201				530		535
202	Pro	Leu	Arg	Leu	Asp	Ala
203				545		550
204	Leu	Glu	Thr	Ile	Leu	Gly
205				565		570
206	Pro	Ser	Ala	Ile	Pro	Thr
207				580		585
208	Pro	Ser	Ser	Ile	Pro	Asp
209				595		600
210	Tyr	Ala	Ser	Gln	Pro	Gly
211				610		615

PAGE: 6

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PATENT APPLICATION US/09/147,346

DATE: 03/22/2000
TIME: 10:17:37

Input Set: I147346.RAW

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